

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 3, 2005, 23:17:42 ; Search time 101 seconds

(without alignments)

3127.531 Million cell updates/sec

Title: US-10-071-838-2

Perfect score: 2983

Sequence: 1 MDVVEVAGSWAQEREDIM..... TSGPCLCGLHLESSQPPGF 549

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 1825181 seqs, 57534646 residues

Total number of hits satisfying chosen parameters:

1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : UniProt 02:*

- 1: uniprot_sprot:*
- 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

ALIGMENTS	
RESULT 1	
TBC3_HUMAN	STANDARD;
ID: Q8T2P1; O9HB9; Q0UDD4;	PRY; 549 AA.
AC: Q8T2P1;	
DT: 10-OCT-2003 (Rel. 42, Created)	
DT: 10-OCT-2003 (Rel. 42, Last sequence update)	
DT: 05-JUL-2005 (Rel. 44, Last annotation update)	
DE: TBC1 domain family member 3 (Rab GTPase-activating protein PRC17)	
DE: (Prostate cancer gene 17 protein) (TRB17 alpha protein).	
GN: Name=TBC1D3; Synonyms=PRC17;	
OS: Homo sapiens (Human);	
OC: Buxarvora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC: Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo.	
ON: NCBI_TaxID=9606;	
RP: SEQUENCE FROM N.A., FUNCTION AND DISEASE.	
RX: MEDLINE-22146263; PubMed=13359748;	
RA: Pei L., Peng Y., Yang Y., Ding X.B., Van Byndhoven W.G., Nguyen K.C.,	
RA: Rubin M., Hoey T., Powers S., Li J.;	
RT: "PRC17, a novel oncogene encoding a Rab GTPase-activating protein, is amplified in prostate cancer.";	
RL: Cancer Res. 62:5420-5424(2002).	
RN: [2]	
RP: SEQUENCE FROM N.A.	
RC: TISSUE-Testis;	
RX: MEDLINE-21154917; PubMed=11230166; DOI=10.1101/gr.154701;	
RA: Wiemann S., Weil B., Wellenreuther R., Gassnerhuber J., Glassl S.,	
RA: Anserge W., Boecker M., Bioecker H., Bauersachs S., Blum H.,	
RA: Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,	
RA: Wambutt R., Korn B., Klein M., Pouska A., Tampe J., Haubner D.,	
Mewes H.-W., Ottewaelde B., Obermaier B.,	
RA: "Towards a catalog of human genes and proteins: sequencing and	
RT: analysis of 500 novel complete protein coding human cDNAs.";	
RT: Genome Res. 11:422-435(2001).	
RN: [3]	
RP: SEQUENCE OF 1-52 FROM N.A.	
RX: MEDLINE-93228825; PubMed=471161;	
RA: Ono M., Nakamura T., Marigo-Samson R., Hill M.;	
RT: "Human TRB17 oncogene is generated from a family of homologous	
RT: polymorphic sequences by single-base changes.";	
RL: Cell Biol. 12:107-118(1993).	
RN: [4]	
RP: SEQUENCE OF 1-52 FROM N.A.	
RT: TISSUE-Placenta;	
RX: MEDLINE-94010310; PubMed=8406013;	
RA: Ono M., Nakamura T., Hill M.;	
RT: "Identification of novel sequences in the repertoire of hypervariable	
RT: TRB17 genes from immortalized normal and malignant human	
RT: keratinocytes.";	
RA: Gene 131:209-215(1993).	
RN: [5]	
RP: TISSUE SPECIFICITY.	
RX: MEDLINE-22506395; PubMed=12604795; DOI=10.1073/pnas.0437015100;	
RA: Paulding C.A., Ruvolo M., Haber D.A.;	

838-2.rup -
Appendix 1, page

RT "The Tre2 (USP6) oncogene is a hominoid-specific gene.";
 RL "Proc. Natl. Acad. Sci. U.S.A. 100:2307-2511(2003)."
 CC -I: FUNCTION: Acts as a GTPase activating protein for RAB5. Does not
 act on RAB4 or RAB11.
 CC -I: TISSUE SPECIFICITY: Expressed in liver, skeletal muscle, kidney,
 pancreas, spleen, testis, ovary, small intestine and peripheral
 blood leukocytes. Overexpressed in prostate cancers.
 CC -I: DISEASE: May be involved in forms of prostate cancer.
 CC -I: SIMILARITY: Contains 1 Rab-GAP TBC domain.

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DR EMBL; AF54053; AAN3117_1; -.
 DR EMBL; AL13666; CAB6679_1; -.
 DR EMBL; X71377; CAB94197_1; -.
 DR Genew; HGNC:19031; TBCD3.
 DR MIM; 607741; -.
 DR InterPro; IPR00195; RabGAP_TBC.
 DR Pfam; PP0566; TBC; 1.
 DR SMART; SM00164; TBC; 1.
 DR PROSITE; PS0086; TBC_RABGAP; 1.
 DR CTPase activation; Proto-oncogene.
 KW Rab-GAP TBC.
 FT DOMAIN 101 293 Rab-GAP TBC.
 FT CONFLICT 117 171 I -> T (in Ref. 2).
 FT CONFLICT 137 137 R -> K (in Ref. 2).
 FT CONFLICT 354 354 Q -> K (in Ref. 2).
 FT CONFLICT 526 526 P -> Q (in Ref. 2).
 SQ SEQUENCE 549 AA; 62168 MW; 831Da747D0B61400 CRC64;

Query Match 100.0%; Score 2983; DB 1; Length 549;
 Best Local Similarity 100.0%; Pred No. 1-48-179;
 Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 MDYVTEVAGSWAQAERDIDMKYKEKRRAGLPEDPKPKPPRSYNNWHDGLVHETBLPL 60	Dy 1 MDYVTEVAGSWAQAERDIDMKYKEKRRAGLPEDPKPKPPRSYNNWHDGLVHETBLPL 60
Qy 61 TARAKQTRBISKSKWADLGEWEKKSSRLIDRAVKMPNMRGPMSVLAIEEM 120	Dy 61 TARAKQTRBISKSKWADLGEWEKKSSRLIDRAVKMPNMRGPMSVLAIEEM 120
Qy 121 KLNKFGRYQIMKEKKRSESHIIQRIDRVGSGTLRKHIFFRDRYRGKORELUHLIAVEEY 180	Dy 121 KLNKFGRYQIMKEKKRSESHIIQRIDRVGSGTLRKHIFFRDRYRGKORELUHLIAVEEY 180
Qy 181 NPEVGYCRDLISHIAALFLYLTPBEDAWFVALLVOLLASERHSLSHGFSPNGTVQGLOQEE 240	Dy 181 NPEVGYCRDLISHIAALFLYLTPBEDAWFVALLVOLLASERHSLSHGFSPNGTVQGLOQEE 240
Qy 241 HVAATSQPKTMGHQDKDQCLCQCSPIGCLIRILIGISLUGITURKDVYLVEGEQALMPI 300	Dy 241 HVAATSQPKTMGHQDKDQCLCQCSPIGCLIRILIGISLUGITURKDVYLVEGEQALMPI 300
Qy 301 TRYAFKVOKRLTKTSRCGWARFENFNUFTWARPDTVQLTRASMKKLTRKQDLP 360	Dy 301 TRYAFKVOKRLTKTSRCGWARFENFNUFTWARPDTVQLTRASMKKLTRKQDLP 360
Qy 361 AKPQQGSSASRPVPVPSRGKGLCKEDRQAPGPPRPPRWSASPPRAPSSTPGGA 420	Dy 361 AKPQQGSSASRPVPVPSRGKGLCKEDRQAPGPPRPPRWSASPPRAPSSTPGGA 420
Qy 421 VREDTYIPVGTVQGVSPALACQGPOOSWRFLAWNHPRLPTDLDVSGPWFRTYDFRSCW 480	Dy 421 VREDTYIPVGTVQGVSPALACQGPOOSWRFLAWNHPRLPTDLDVSGPWFRTYDFRSCW 480
Qy 481 RAISCDQDQAPCWQDEHPAEPVRSFAAPSTDSDQCTPFRARDCPCAPSGPCICLGLHL 540	Dy 481 RAISCDQDQAPCWQDEHPAEPVRSFAAPSTDSDQCTPFRARDCPCAPSGPCICLGLHL 540

RESULT 2						
QY	541	ESSOPPGF	549			
Db	541	ESSOPPGF	549			
QY	601PXL	PRELIMINARY;	PRT;	549 AA.		
AC	Q61PXL1;					
DT	05-JUL-2004	(Tremblel.	27, Created)			
DT	05-Jul-2004	(Tremblel.	27, Last sequence update)			
DE	TBC1 domain family, member 3.					
GN	Name=TBCD3;					
OS	Homo sapiens (Human).					
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	{1}					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Brain;					
RA	Medline:2238857; PubMed=12477932;					
RA	Strausberg R.L., Palingd E.A., Grouse L.H., Derge J.G.,					
RA	Klauber R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,					
RA	Altenschul S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Bhat N.K.,					
RA	Hopkins R.F., Jordon H., Moore T., Max S.I., Wang J., Haieh P.,					
RA	Diamond L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,					
RA	Rana S.S., Loucellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,					
RA	Bosak S.A., McElwain J.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,					
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,					
RA	Villalon D.M., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Faney J., Heitton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,					
RA	Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA	Rodriguez A.C., Grindham J.J., Schmutz J., Myers R.M., Butterfield Y.S.,					
RA	Krzewinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B.,					
RA	Jones S.J., Marras M.A.; "Generation and initial analysis of more than 15,000 full-length human					
RT	and mouse cDNA sequences", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Brain;					
RA	Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.					
DR	EMBL: BC071680; AAH11680.1; -.					
DR	InterPro: IPR00195; RabGAP_TBC.					
DR	PFam: PF00566; TBC; 1.					
DR	SMART: SNO016A; TBC; 1.					
DR	PROSITE: PS50086; TBC_RABGAP; 1.					
SQ	SEQUENCE 549 AA; 62231 MW; 5657E5602B3655P5 CRC64;					
Query	Query Match 99.6%; Score 2971; DB 2; Length 549;					
QY	Best Local Similarity 99.5%; Pred. No. 8.2e-179; Mismatches 546; Conservative 2; Mismatches 1; Indels 0; Gaps 0;					
Db	1 MDVVVAGWAGWAQEBEDIMIIVKVEKSRKGHRAGLEPDKGKPKFRSTNNWDHLGIVETELPL 60					
Db	1 MDVVVAGWAGWAQEBEDIMIIVKVEKSRKGHRAGLEPDKGKPKFRSTNNWDHLGIVETELPL 60					
QY	61 TAREKQKIREBISRSKSKVWDMLGDKWRYKKSRSRKLIDRAYKGPMNIRGPWMNSVILNTLEM 120					
QY	61 TAREKQKIREBISRSKSKVWDMLGDKWRYKKSRSRKLIDRAYKGPMNIRGPWMNSVILNTLEM 120					
Db	121 KLNKNPGRYQIMKEKKRSSEHIQDRDVSGTIRKUJFPRDRYGTKORELLHILLAYREY 180					
Db	121 KLNKNPGRYQIMKEKKRSSEHIQDRDVSGTIRKUJFPRDRYGTKORELLHILLAYREY 180					
QY	181 NPEVGCRDISHIAALFLYVPEEDAFWALVOLLASERBSHLSQFGHSPNGGTVOGLQDOE 240					